

# Phyre2

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 Description RVBD1636\_(TB15.3)\_1842458\_1842898  
 Date Fri Aug 2 13:30:23 BST 2019  
 Unique Job ID 3fd0f9e3501a9aa6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1tq8a_</a>	Alignment		99.9	97	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Universal stress protein-like
2	<a href="#">c5ahwC_</a>	Alignment		99.9	69	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> universal stress protein; <b>PDBTitle:</b> crystal structure of universal stress protein msmeg_3811 in2 complex with camp
3	<a href="#">c3s3tD_</a>	Alignment		99.9	19	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> nucleotide-binding protein, universal stress protein uspa <b>PDBTitle:</b> universal stress protein uspa from lactobacillus plantarum
4	<a href="#">c3hgmD_</a>	Alignment		99.9	21	<b>PDB header:</b> signaling protein <b>Chain:</b> D: <b>PDB Molecule:</b> universal stress protein tead; <b>PDBTitle:</b> universal stress protein tead from the trap transporter teaabc of2 halomonas elongata
5	<a href="#">d2z3va1</a>	Alignment		99.9	26	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Universal stress protein-like
6	<a href="#">d1mjha_</a>	Alignment		99.9	24	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Universal stress protein-like
7	<a href="#">c3dloC_</a>	Alignment		99.9	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> universal stress protein; <b>PDBTitle:</b> structure of universal stress protein from archaeoglobus fulgidus
8	<a href="#">c3olqA_</a>	Alignment		99.9	28	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> universal stress protein e; <b>PDBTitle:</b> the crystal structure of a universal stress protein e from proteus2 mirabilis hi4320
9	<a href="#">c3fg9B_</a>	Alignment		99.9	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> protein of universal stress protein uspa family; <b>PDBTitle:</b> the crystal structure of an universal stress protein uspa2 family protein from lactobacillus plantarum wcfs1
10	<a href="#">d1jmva_</a>	Alignment		99.9	21	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Universal stress protein-like
11	<a href="#">c4wnyA_</a>	Alignment		99.9	21	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> universal stress protein; <b>PDBTitle:</b> crystal structure of a protein from the universal stress protein2 family from burkholderia pseudomallei

12	<a href="#">c2dumD_</a>	Alignment		99.9	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> hypothetical protein ph0823; <b>PDBTitle:</b> crystal structure of hypothetical protein, ph0823
13	<a href="#">d2gm3a1</a>	Alignment		99.9	23	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Universal stress protein-like
14	<a href="#">c3fh0A_</a>	Alignment		99.8	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative universal stress protein kpn_01444; <b>PDBTitle:</b> crystal structure of putative universal stress protein kpn_01444 -2 atpase
15	<a href="#">c2pfsA_</a>	Alignment		99.8	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> universal stress protein; <b>PDBTitle:</b> crystal structure of universal stress protein from nitrosomonas2 europaea
16	<a href="#">c4r2B_</a>	Alignment		99.8	22	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> universal stress protein f; <b>PDBTitle:</b> crystal structure of ynaf (universal stress protein f) from salmonella2 typhimurium
17	<a href="#">c4r2jA_</a>	Alignment		99.8	11	<b>PDB header:</b> metal binding protein, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> universal stress protein e; <b>PDBTitle:</b> crystal structure of ydaa (universal stress protein e) from salmonella2 typhimurium
18	<a href="#">c3loqA_</a>	Alignment		99.8	23	<b>PDB header:</b> structure genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> universal stress protein; <b>PDBTitle:</b> the crystal structure of a universal stress protein from archaeoglobus2 fulgidus dsm 4304
19	<a href="#">c3idfA_</a>	Alignment		99.8	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> usp-like protein; <b>PDBTitle:</b> the crystal structure of a usp-like protein from wolinnella2 succinogenes to 2.0a
20	<a href="#">d1q77a_</a>	Alignment		99.8	16	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Universal stress protein-like
21	<a href="#">c3mt0A_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein pa1789; <b>PDBTitle:</b> the crystal structure of a functionally unknown protein pa1789 from2 pseudomonas aeruginosa pao1
22	<a href="#">c2jaxA_</a>	Alignment	not modelled	99.7	24	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein tb31.7; <b>PDBTitle:</b> universal stress protein rv2623 from mycobacterium2 tuberculosis
23	<a href="#">c3ab8B_</a>	Alignment	not modelled	99.7	26	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative uncharacterized protein ttha0350; <b>PDBTitle:</b> crystal structure of the hypothetical tandem-type universal stress2 protein ttha0350 complexed with atps.
24	<a href="#">c5ol2E_</a>	Alignment	not modelled	95.2	11	<b>PDB header:</b> flavoprotein <b>Chain:</b> E: <b>PDB Molecule:</b> electron transfer flavoprotein small subunit; <b>PDBTitle:</b> the electron transferring flavoprotein/butyryl-coa dehydrogenase2 complex from clostridium difficile
25	<a href="#">c5ow0B_</a>	Alignment	not modelled	94.0	16	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> electron transfer flavoprotein, beta subunit; <b>PDBTitle:</b> crystal structure of an electron transfer flavoprotein from2 geobacillus metallireducens
26	<a href="#">d1o94c_</a>	Alignment	not modelled	93.9	13	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> ETFP subunits
27	<a href="#">d3clsc1</a>	Alignment	not modelled	93.4	12	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> ETFP subunits
						<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> caffeyl-coa reductase-etf complex subunit

28	<a href="#">c6fahB_</a>	Alignment	not modelled	92.2	12	card; <b>PDBTitle:</b> molecular basis of the flavin-based electron-bifurcating caffeyl-coa2 reductase reaction
29	<a href="#">c4kpuB_</a>	Alignment	not modelled	92.0	12	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> electron transfer flavoprotein alpha/beta-subunit; <b>PDBTitle:</b> electron transferring flavoprotein of acidaminococcus fermentans:2 towards a mechanism of flavin-based electron bifurcation
30	<a href="#">d1efvb_</a>	Alignment	not modelled	91.8	19	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> ETFP subunits
31	<a href="#">d1wy5a1</a>	Alignment	not modelled	90.2	17	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> PP-loop ATPase
32	<a href="#">d1efpb_</a>	Alignment	not modelled	89.6	22	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> ETFP subunits
33	<a href="#">c4I2iA_</a>	Alignment	not modelled	86.7	17	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> electron transfer flavoprotein alpha subunit; <b>PDBTitle:</b> electron transferring flavoprotein of acidaminococcus fermentans:2 towards a mechanism of flavin-based electron bifurcation
34	<a href="#">c5gafi_</a>	Alignment	not modelled	86.1	18	<b>PDB header:</b> ribosome <b>Chain:</b> I: <b>PDB Molecule:</b> 50s ribosomal protein I10; <b>PDBTitle:</b> rnc in complex with srp
35	<a href="#">c3zquA_</a>	Alignment	not modelled	80.3	8	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> probable aromatic acid decarboxylase; <b>PDBTitle:</b> structure of a probable aromatic acid decarboxylase
36	<a href="#">c3a2kB_</a>	Alignment	not modelled	77.9	17	<b>PDB header:</b> ligase/rna <b>Chain:</b> B: <b>PDB Molecule:</b> trna(ile)-lysine synthase; <b>PDBTitle:</b> crystal structure of tils complexed with trna
37	<a href="#">c2j289_</a>	Alignment	not modelled	72.9	17	<b>PDB header:</b> ribosome <b>Chain:</b> 9: <b>PDB Molecule:</b> signal recognition particle 54; <b>PDBTitle:</b> model of e. coli srp bound to 70s rncs
38	<a href="#">c1o94D_</a>	Alignment	not modelled	72.4	12	<b>PDB header:</b> electron transport <b>Chain:</b> D: <b>PDB Molecule:</b> electron transfer flavoprotein alpha-subunit; <b>PDBTitle:</b> ternary complex between trimethylamine dehydrogenase and2 electron transferring flavoprotein
39	<a href="#">c2e21A_</a>	Alignment	not modelled	68.8	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> trna(ile)-lysine synthase; <b>PDBTitle:</b> crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
40	<a href="#">d2ielea1</a>	Alignment	not modelled	65.5	13	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Universal stress protein-like
41	<a href="#">c2iy3A_</a>	Alignment	not modelled	59.8	24	<b>PDB header:</b> rna-binding <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle protein,signal recognition <b>PDBTitle:</b> structure of the e. coli signal recognition particle
42	<a href="#">c6jddA_</a>	Alignment	not modelled	58.2	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> cypemycin cysteine dehydrogenase (decarboxylating); <b>PDBTitle:</b> crystal structure of the cypemycin decarboxylase cypd.
43	<a href="#">d1rvga_</a>	Alignment	not modelled	58.0	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class II FBP aldolase
44	<a href="#">c3ih5A_</a>	Alignment	not modelled	57.7	18	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> electron transfer flavoprotein alpha-subunit; <b>PDBTitle:</b> crystal structure of electron transfer flavoprotein alpha-subunit from2 bacteroides thetaiotaomicron
45	<a href="#">d1g5qa_</a>	Alignment	not modelled	57.5	9	<b>Fold:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Superfamily:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Family:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
46	<a href="#">c4u7jB_</a>	Alignment	not modelled	56.3	16	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> argininosuccinate synthase; <b>PDBTitle:</b> crystal structure of argininosuccinate synthase from mycobacterium2 thermoresistibile
47	<a href="#">c6fahE_</a>	Alignment	not modelled	55.9	13	<b>PDB header:</b> flavoprotein <b>Chain:</b> E: <b>PDB Molecule:</b> caffeyl-coa reductase-etf complex subunit care; <b>PDBTitle:</b> molecular basis of the flavin-based electron-bifurcating caffeyl-coa2 reductase reaction
48	<a href="#">c2j37W_</a>	Alignment	not modelled	54.5	16	<b>PDB header:</b> ribosome <b>Chain:</b> W: <b>PDB Molecule:</b> signal recognition particle 54 kda protein (srp54); <b>PDBTitle:</b> model of mammalian srp bound to 80s rncs
49	<a href="#">c2ejbA_</a>	Alignment	not modelled	51.4	6	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> probable aromatic acid decarboxylase; <b>PDBTitle:</b> crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
50	<a href="#">d1p3y1_</a>	Alignment	not modelled	50.8	16	<b>Fold:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Superfamily:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Family:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
51	<a href="#">c5udwB_</a>	Alignment	not modelled	49.9	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> lactate racemization operon protein lare; <b>PDBTitle:</b> lare, a sulfur transferase involved in synthesis of the cofactor for2 lactate racemase, in complex with nickel
52	<a href="#">c6oaA_</a>	Alignment	not modelled	48.1	24	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> phosphopantothenoilcysteine

52	<a href="#">c6v6a_</a>	Alignment	not modelled	48.1	24	decarboxylase; <b>PDBTitle:</b> crystal structure of hal3 from cryptococcus neoformans
53	<a href="#">d1qzua_</a>	Alignment	not modelled	47.9	17	<b>Fold:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Superfamily:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Family:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
54	<a href="#">c3qjgD_</a>	Alignment	not modelled	46.9	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> epidermin biosynthesis protein epid; <b>PDBTitle:</b> epidermin biosynthesis protein epid from staphylococcus aureus
55	<a href="#">d3clsd1</a>	Alignment	not modelled	46.6	14	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> ETFP subunits
56	<a href="#">c3dm5A_</a>	Alignment	not modelled	45.3	15	<b>PDB header:</b> rna binding protein, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition 54 kda protein; <b>PDBTitle:</b> structures of srp54 and srp19, the two proteins assembling the 2 ribonucleic core of the signal recognition particle from the archaeon 3 pyrococcus furiosus.
57	<a href="#">c6qlgD_</a>	Alignment	not modelled	44.8	12	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> flavin prenyltransferase pad1, mitochondrial; <b>PDBTitle:</b> crystal structure of anubix (pada1) in complex with fm n and 2 dimethylallyl pyrophosphate
58	<a href="#">c6ofuC_</a>	Alignment	not modelled	44.5	12	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> ydji aldolase; <b>PDBTitle:</b> x-ray crystal structure of the ydji aldolase from escherichia coli k12
59	<a href="#">c4nzpA_</a>	Alignment	not modelled	44.0	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> argininosuccinate synthase; <b>PDBTitle:</b> the crystal structure of argininosuccinate synthase from campylobacter 2 jejuni subsp. jejuni nctc 11168
60	<a href="#">d1j20a1</a>	Alignment	not modelled	43.9	15	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
61	<a href="#">d2dbsa1</a>	Alignment	not modelled	43.4	20	<b>Fold:</b> TTHC002-like <b>Superfamily:</b> TTHC002-like <b>Family:</b> TTHC002-like
62	<a href="#">c5h75B_</a>	Alignment	not modelled	42.8	18	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> mersacidin decarboxylase,immunoglobulin g-binding protein <b>PDBTitle:</b> crystal structure of the mrsd-protein a fusion protein
63	<a href="#">c4rheB_</a>	Alignment	not modelled	41.4	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-octaprenyl-4-hydroxybenzoate carboxy-lyase; <b>PDBTitle:</b> crystal structure of ubix, an aromatic acid decarboxylase from the 2 colwellia psychrerythraea 34h
64	<a href="#">d1zuna1</a>	Alignment	not modelled	41.0	7	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> PAPS reductase-like
65	<a href="#">c2xdqB_</a>	Alignment	not modelled	40.3	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> light-independent protochlorophyllide reductase subunit b; <b>PDBTitle:</b> dark operative protochlorophyllide oxidoreductase (chl-chlb)2 complex
66	<a href="#">c3pm6B_</a>	Alignment	not modelled	39.9	14	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative fructose-bisphosphate aldolase; <b>PDBTitle:</b> crystal structure of a putative fructose-1,6-biphosphate aldolase from 2 coccidioides immitis solved by combined sad mr
67	<a href="#">d1nu0a_</a>	Alignment	not modelled	39.6	18	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Putative Holliday junction resolvase RuvX
68	<a href="#">c3mcuF_</a>	Alignment	not modelled	38.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> dipicolinate synthase, b chain; <b>PDBTitle:</b> crystal structure of the dipicolinate synthase chain b from bacillus 2 cereus. northeast structural genomics consortium target bcr215.
69	<a href="#">d1gvfa_</a>	Alignment	not modelled	37.4	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class II FBP aldolase
70	<a href="#">c1ni5A_</a>	Alignment	not modelled	35.8	19	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> putative cell cycle protein mesj; <b>PDBTitle:</b> structure of the mesj pp-atpase from escherichia coli
71	<a href="#">c3clrD_</a>	Alignment	not modelled	34.3	12	<b>PDB header:</b> electron transport <b>Chain:</b> D: <b>PDB Molecule:</b> electron transfer flavoprotein subunit alpha; <b>PDBTitle:</b> crystal structure of the r236a etf mutant from m. methylotrophus
72	<a href="#">c3pdiG_</a>	Alignment	not modelled	30.8	15	<b>PDB header:</b> protein binding <b>Chain:</b> G: <b>PDB Molecule:</b> nitrogenase mofe cofactor biosynthesis protein nife; <b>PDBTitle:</b> precursor bound nifen
73	<a href="#">c1zunA_</a>	Alignment	not modelled	30.6	7	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfate adenylyltransferase subunit 2; <b>PDBTitle:</b> crystal structure of a gtp-regulated atp sulfurylase 2 heterodimer from pseudomonas syringae
74	<a href="#">c2xdqA_</a>	Alignment	not modelled	30.4	6	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> light-independent protochlorophyllide reductase subunit n; <b>PDBTitle:</b> dark operative protochlorophyllide oxidoreductase (chl-chlb)2 complex
75	<a href="#">d1dd9a_</a>	Alignment	not modelled	30.0	13	<b>Fold:</b> DNA primase core <b>Superfamily:</b> DNA primase core <b>Family:</b> DNA primase DnaG catalytic core
76	<a href="#">c1dd9A_</a>	Alignment	not modelled	30.0	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna primase; <b>PDBTitle:</b> structure of the dnaG catalytic core

77	<a href="#">c1k97A_</a>	Alignment	not modelled	29.9	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> argininosuccinate synthase; <b>PDBTitle:</b> crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline
78	<a href="#">d1t6t1_</a>	Alignment	not modelled	29.8	11	<b>Fold:</b> Toprim domain <b>Superfamily:</b> Toprim domain <b>Family:</b> Toprim domain
79	<a href="#">d1sbza_</a>	Alignment	not modelled	29.1	11	<b>Fold:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Superfamily:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Family:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
80	<a href="#">c6jlsA_</a>	Alignment	not modelled	28.6	23	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative flavoprotein decarboxylase; <b>PDBTitle:</b> crystal structure of fmn-dependent cysteine decarboxylases tvaf from2 thioviridamide biosynthesis
81	<a href="#">c3vrhA_</a>	Alignment	not modelled	26.7	19	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein ph0300; <b>PDBTitle:</b> crystal structure of ph0300
82	<a href="#">d1uyra2</a>	Alignment	not modelled	26.6	16	<b>Fold:</b> ClpP/crotonase <b>Superfamily:</b> ClpP/crotonase <b>Family:</b> Biotin dependent carboxylase carboxyltransferase domain
83	<a href="#">c3tvsA_</a>	Alignment	not modelled	26.5	11	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> cryptochrome-1; <b>PDBTitle:</b> structure of full-length drosophila cryptochrome
84	<a href="#">c4qskB_</a>	Alignment	not modelled	26.0	14	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate carboxylase; <b>PDBTitle:</b> crystal structure of l. monocytogenes pyruvate carboxylase in complex2 with cyclic-di-amp
85	<a href="#">d1gph11</a>	Alignment	not modelled	24.3	12	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
86	<a href="#">d1gsoa2</a>	Alignment	not modelled	23.7	50	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
87	<a href="#">d1vbka1</a>	Alignment	not modelled	23.2	11	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Thil-like
88	<a href="#">c3iv7B_</a>	Alignment	not modelled	21.2	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alcohol dehydrogenase iv; <b>PDBTitle:</b> crystal structure of iron-containing alcohol dehydrogenase2 (np_602249.1) from corynebacterium glutamicum atcc 13032 kitasato at3 2.07 a resolution
89	<a href="#">c2v3cC_</a>	Alignment	not modelled	21.1	23	<b>PDB header:</b> signaling protein <b>Chain:</b> C: <b>PDB Molecule:</b> signal recognition 54 kda protein; <b>PDBTitle:</b> crystal structure of the srp54-srp19-7s.s srp rna complex2 of m. jannaschii
90	<a href="#">c5l3rC_</a>	Alignment	not modelled	20.9	17	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> signal recognition particle 54 kda protein, chloroplastic; <b>PDBTitle:</b> structure of the gtpase heterodimer of chloroplast srp54 and ftsy from2 arabidopsis thaliana
91	<a href="#">d1ecfa1</a>	Alignment	not modelled	20.7	12	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
92	<a href="#">d1xkya1</a>	Alignment	not modelled	20.5	9	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
93	<a href="#">d1mvla_</a>	Alignment	not modelled	20.5	12	<b>Fold:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Superfamily:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD <b>Family:</b> Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
94	<a href="#">c1mvlA_</a>	Alignment	not modelled	20.5	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> ppc decarboxylase athal3a; <b>PDBTitle:</b> ppc decarboxylase mutant c175s
95	<a href="#">c2j7pA_</a>	Alignment	not modelled	20.4	25	<b>PDB header:</b> signal recognition <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle protein; <b>PDBTitle:</b> gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
96	<a href="#">d1nuia1</a>	Alignment	not modelled	20.0	20	<b>Fold:</b> DNA primase core <b>Superfamily:</b> DNA primase core <b>Family:</b> Primase fragment of primase-helicase protein
97	<a href="#">d3bzka5</a>	Alignment	not modelled	20.0	21	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Ribonuclease H-like <b>Family:</b> Tex RuvX-like domain-like
98	<a href="#">d1ru8a_</a>	Alignment	not modelled	19.9	18	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> N-type ATP pyrophosphatases
99	<a href="#">c5l3sF_</a>	Alignment	not modelled	19.8	12	<b>PDB header:</b> protein transport <b>Chain:</b> F: <b>PDB Molecule:</b> signal recognition particle receptor ftsy; <b>PDBTitle:</b> structure of the gtpase heterodimer of crenarchaeal srp54 and ftsy